VERSION WITH MARKINGS TO SHOW CHANGES MADE

Cancel Claims 10-32 and 34-49.

Please enter the following new claims:

--50. A hybridization assay comprising:

(a) contacting a sample of target nucleic acids under hybridization conditions that require a target nucleic acid of 14 nucleotides in length to have at least 70% sequence identity with a probe in order to hybridize to said probe with a collection of substrate bound probe nucleic acid features that includes at least one background nucleic acid feature that minimally binds to its complementary target under said hybridization conditions; and

(b) detecting the presence of target nucleic acids hybridized to said collection of probe nucleic acid features.

51. The hybridization assay according to Claim 50, wherein said sample of target nucleic acids is labeled with a detectable label prior to said contacting step.

52. The hybridization assay according to Claim 50, wherein said sample of target nucleic acids is labeled with a detectable label between said contacting and detecting steps.

53. The hybridization according to Claim 50, wherein said method further comprises a washing step between said contacting and detecting steps.

54. The method according to Claim 50, wherein said method further comprises subtracting a detected signal from said at least one background feature from signal detected from any other probe nucleic acid feature of said collection of substrate bound probe nucleic acid features.

55. The method according to Claim 50, wherein said collection of substrate bound probe nucleic acid features is an array of nucleic acid features.

56. The method according to Claim 50, wherein said hybridization assay is a method of estimating the background noise in a hybridization assay.

57. The method according to Claim 50, wherein said method is a method of validating a test background feature.

58. A hybridization assay comprising:

(a) contacting a sample of target nucleic acids under hybridization conditions that require a target nucleic acid of 14 nucleotides in length to have at least 70% sequence identity with a probe in order to hybridize to said probe with a collection of substrate bound probe nucleic acid features that includes at least one background nucleic acid feature, wherein said at least one background feature is made up of a probe nucleic acid selected from the group consisting of SEQ ID NOS: 05 to 32 or a probe that similarly minimally binds to an R6G-labeled yeast cRNA target pool according to the test assay described in Example 3.B.; and

(b) detecting the presence of target nucleic acids hybridized to said collection of probe nucleic acid features.

59. A hybridization assay comprising:

(a) contacting a sample of target nucleic acids under hybridization conditions that require a target nucleic acid of 14 nucleotides in length to have at least 70% sequence identity with a probe in order to hybridize to said probe with a collection of substrate bound probe nucleic acid features that includes at least one background nucleic acid feature, wherein said at least one background feature is made up of a probe nucleic acid that minimally binds to an R6G-labeled yeast cRNA target pool according to the test assay described in Example 3.B.; and

(b) detecting the presence of target nucleic acids hybridized to said collection of probe nucleic acid features.

60. A hybridization assay comprising:

(a) contacting a sample of detectably labeled target nucleic acids under hybridization conditions that require a target nucleic acid of 14 nucleotides in length to have at least 70% sequence identity with a probe in order to hybridize to said probe with an array

of probe nucleic acid features that includes at least one background nucleic acid feature that minimally binds to its complementary target under said hybridization conditions;

(b) separating non-hybridized target nucleic acids from said array; and

(c) detecting the presence of target nucleic acids hybridized to said array probe nucleic acid features.

61. The method according to Claim 60, wherein said method further comprises subtracting a detected signal from said at least one background feature from signal detected from any other probe nucleic acid feature of said array.

62. A hybridization assay comprising:

(a) contacting a sample of detectably labeled target nucleic acids under hybridization conditions that require a target nucleic acid of 14 nucleotides in length to have at least 70% sequence identity with a probe in order to hybridize to said probe with an array of probe nucleic acid features that includes at least one background nucleic acid feature, wherein said at least one background feature is made up of a probe nucleic acid selected from the group consisting of SEQ ID NOS: 05 to 32 or a probe that similarly minimally binds to an R6G-labeled yeast cRNA target pool according to the test assay described in Example 3.B.;

(b) separating non-hybridized target nucleic acids from said array; and

(c) detecting the presence of target nucleic acids hybridized to said array probe nucleic acid features.

63. A hybridization assay comprising:

(a) contacting a sample of detectably labeled target nucleic acids under hybridization conditions that require a target nucleic acid of 14 nucleotides in length to have at least 70% sequence identity with a probe in order to hybridize to said probe with an array of probe nucleic acid features that includes at least one background nucleic acid feature, wherein said at least one background feature is made up of a probe nucleic acid that minimally binds to an R6G-labeled yeast cRNA target pool according to the test assay described in Example 3.B.;

(b) separating non-hybridized target nucleic acids from said array; and

(c) detecting the presence of target nucleic acids hybridized to said array probe nucleic acid features.

64. A hybridization assay comprising:

(a) contacting a sample of target nucleic acids under hybridization conditions that require a target nucleic acid of 14 nucleotides in length to have at least 70% sequence identity with a probe in order to hybridize to said probe with an array of probe nucleic acid features that includes at least one background nucleic acid feature that minimally binds to its complementary target under said hybridization conditions;

(b) separating non-hybridized target nucleic acids from said array;

(c) detectably labeling target nucleic acids hybridized to said array of probe nucleic acid features; and

(d) detecting the presence of target nucleic acids hybridized to said array of probe nucleic acid features.

65. The method according to Claim 64, wherein said method further comprises subtracting a detected signal from said at least one background feature from signal detected from any other probe nucleic acid feature of said array.

66. A hybridization assay comprising:

(a) contacting a sample of target nucleic acids under hybridization conditions that require a target nucleic acid of 14 nucleotides in length to have at least 70% sequence identity with a probe in order to hybridize to said probe with an array of probe nucleic acid features that includes at least one background nucleic acid feature, wherein said at least one background feature is made up of a probe nucleic acid selected from the group consisting of SEQ ID NOS: 05 to 32 or a probe that similarly minimally binds to an R6G-labeled yeast cRNA target pool according to the test assay described in Example 3.B.;

(b) separating non-hybridized target nucleic acids from said array;

(c) detectably labeling target nucleic acids hybridized to said array of probe nucleic acid features; and

(d) detecting the presence of target nucleic acids hybridized to said array of probe nucleic acid features.

67. A hybridization assay comprising:

(a) contacting a sample of target nucleic acids under hybridization conditions that require a target nucleic acid of 14 nucleotides in length to have at least 70% sequence identity with a probe in order to hybridize to said probe with an array of probe nucleic acid features that includes at least one background nucleic acid feature, wherein said at least one background feature is made up of a probe nucleic acid that minimally binds to an R6G-labeled yeast cRNA target pool according to the test assay described in Example 3.B.;

(b) separating non-hybridized target nucleic acids from said array;

(c) detectably labeling target nucleic acids hybridized to said array of probe nucleic acid features; and

(d) detecting the presence of target nucleic acids hybridized to said array of probe nucleic acid features.

68. A kit for use in a hybridization assay, said kit comprising:

a collection of substrate bound probe nucleic acid features that includes at least one background nucleic acid feature that minimally binds to its complementary target under hybridization conditions that require a target nucleic acid of 14 nucleotides in length to have at least 70% sequence identity with a probe in order to hybridize to said probe.

69. The kit according to Claim 68, wherein said at least one background feature is made up of a probe nucleic acid selected from the group consisting of SEQ ID NOS: 05 to 32 or a probe that similarly minimally binds to an R6G-labeled yeast cRNA target pool according to the test assay described in Example 3.B.

70. The kit according to Claim 69, wherein said at least one background feature is made up of a probe nucleic acid that minimally binds to an R6G-labeled yeast cRNA target pool according to the test assay described in Example 3.B.

71. A hybridization assay comprising:

(a) contacting a sample of target nucleic acids under hybridization conditions that require a target nucleic acid of 14 nucleotides in length to have at least 70% sequence identity with a probe in order to hybridize to said probe with a collection of substrate bound probe nucleic acid features that includes at least one background nucleic acid feature made up of background probes that do not selectively bind to any of said target nucleic acids; and

(b) detecting the presence of target nucleic acids hybridized to said collection of probe nucleic acid features.

72. The hybridization assay according to Claim 71, wherein said sample of target nucleic acids is labeled with a detectable label prior to said contacting step.

73. The hybridization assay according to Claim 71, wherein said sample of target nucleic acids is labeled with a detectable label between said contacting and detecting steps.

74. The hybridization according to Claim 71, wherein said method further comprises a washing step between said contacting and detecting steps.

75. The method according to Claim 71, wherein said method further comprises subtracting a detected signal from said at least one background feature from signal detected from any other probe nucleic acid feature of said collection of substrate bound probe nucleic acid features.

76. The method according to Claim 71, wherein said collection of substrate bound probe nucleic acid features is an array of nucleic acid features.

77. The method according to Claim 71, wherein said hybridization assay is a method of estimating the background noise in a hybridization assay.

78. The method according to Claim 71, wherein said method is a method of validating a test background feature. --